



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

DK

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/142,471	11/04/98	ROSE-JOHN	S 012627-009

021839 HM22/0222
BURNS DOANE SWECKER & MATHIS
P O BOX 1404
ALEXANDRIA VA 22313-1404

EXAMINER

O HARA, E

ART UNIT	PAPER NUMBER
----------	--------------

1646

10

DATE MAILED:

02/22/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/142,471	11/4/98	Stefan Rose-John	012627-009

EXAMINER	
Eileen B. O'Hara	
ART UNIT	PAPER NUMBER
1646	10

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The response filed on Jan. 4, 2000 is not fully responsive to the Office action mailed Aug. 4, 1999, because the computer readable form (CRF) of the sequence listing could not be processed by the Scientific and Technical Information Center (STIC) for the reasons set forth on the attached Raw Sequence Listing Error Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is required to complete the response within a time limit of one (1) month from the date of this letter or within the time remaining in the response period of the communication mailed [mail date], whichever is the longer. 37 CFR 1.135(c).

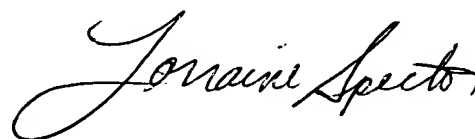
NO EXTENSION OF THIS TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. 1.136(a) OR (b), BUT THE STATUTORY PERIOD FOR RESPONSE SET IN THE COMMUNICATION MAILED [mail date] MAY BE EXTENDED UP TO A MAXIMUM OF SIX (6) MONTHS UNDER 37 CFR 1.136.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Eileen B. O'Hara, whose telephone number is (703) 308-3312. The examiner can normally be reached on Monday through Friday from 9:00 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Kunz can be reached at (703) 308-4623.

Official papers filed by fax should be directed to (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.



LORRAINE SPECTOR
PRIMARY EXAMINER

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/142,471

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) 2 (maybe). Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

E. O. Hara

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000
TIME: 11:45:43

Input Set: I142471.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Need

P.3

```
1 <110> APPLICANT: ROEWKAMP, Walter
2 ROSE-JOHN, Stefan
3 <120> TITLE OF INVENTION: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
4 <130> FILE REFERENCE: 012627-009
5 <140> CURRENT APPLICATION NUMBER: US/09/142,471
6 <141> CURRENT FILING DATE: 1998-11-04
7 <150> EARLIER APPLICATION NUMBER: PCT/DE97/00458
8 <151> EARLIER FILING DATE: 1997-03-07
9 <150> EARLIER APPLICATION NUMBER: DE 196 08 813.5
10 <151> EARLIER FILING DATE: 1996-03-07
11 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 1627
15 <212> TYPE: DNA
16 <213> ORGANISM: Unknown
17 <220> FEATURE:
18 <221> NAME/KEY: sig_peptide
19 <222> LOCATION: (34)..(90)
20 <220> FEATURE:
21 <221> NAME/KEY: mat_peptide
22 <222> LOCATION: (91)..(1608)
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (34)..(1608)
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
28 comprising two polypeptides with a mutual
29 affinity.
30 <400> SEQUENCE: 1
31 gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
32 Met Leu Ala Val Gly Cys Ala
33 -15
34 ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
35 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
36 -10 -5 -1 1
37 cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
38 Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
39 5 10 15 20
40 gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
41 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
42 25 30 35
43 gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
44 Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
```

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000
TIME: 11:45:43

Input Set: I142471.RAW

45		40		45		50		
46	agc	aga	tgg	gct	ggc	atg	gga	agg
47	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg
48			55				60	
49	ctc	cac	gac	tct	gga	aac	tat	tca
50	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser
51			70				75	
52	ggg	act	gtg	cac	ttg	ctg	gtg	gat
53	Gly	Thr	Val	His	Leu	Leu	Val	Asp
54			85				90	
55	tcc	tgc	ttc	cgg	aag	agc	ccc	ctc
56	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu
57							105	
58	cct	cgg	agc	acc	cca	tcc	ctg	acg
59	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr
60							120	
61	aag	ttt	cag	aac	agt	ccg	gcc	gaa
62	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu
63							135	
64	tcc	cag	gag	tcc	cag	aag	ttc	tcc
65	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser
66							150	
67	gac	agc	tct	ttc	tac	ata	gtg	tcc
68	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser
69							165	
70	agc	aag	ttc	agc	aaa	act	caa	acc
71	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr
72							185	
73	cct	gat	ccg	cct	gcc	aac	atc	aca
74	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr
75							200	
76	cgc	tgg	ctc	agt	gtc	acc	tgg	caa
77	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln
78							215	
79	ttc	tac	aga	cta	cgg	ttt	gag	ctc
80	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu
81							230	
82	aca	ttc	aca	aca	tgg	atg	gtc	aag
83	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys
84							245	
85	cac	gac	gcc	tgg	agc	ggc	ctg	agg
86	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg
87							265	
88	gag	gag	ttc	ggg	caa	ggc	gag	tgg
89	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp
90							280	
91	ggc	acg	cct	tgg	aca	gaa	tcc	agg
92	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg
93							295	
94	ggg	tct	gga	ggg	gga	ggg	tct	gga

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/142,471

 DATE: 01/28/2000
 TIME: 11:45:43

Input Set: I142471.RAW

95	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val	Glu	Pro	Val	
96		310					315					320					
97	ccc	cca	gga	gaa	gat	tcc	aaa	gat	gta	gcc	gcc	cca	cac	aga	cag	cca	1110
98	Pro	Pro	Gly	Glu	Asp	Ser	Lys	Asp	Val	Ala	Ala	Pro	His	Arg	Gln	Pro	
99	325					330				335					340		
100	ctc	acc	tct	tca	gaa	cga	att	gac	aaa	caa	att	cgg	tac	atc	ctc	gac	1158
101	Leu	Thr	Ser	Ser	Glu	Arg	Ile	Asp	Lys	Gln	Ile	Arg	Tyr	Ile	Leu	Asp	
102					345					350					355		
103	ggc	atc	tca	gcc	ctg	aga	aag	gag	aca	tgt	aac	aag	agt	aac	atg	tgt	1206
104	Gly	Ile	Ser	Ala	Leu	Arg	Lys	Glu	Thr	Cys	Asn	Lys	Ser	Asn	Met	Cys	
105				360					365					370			
106	gaa	agc	agc	aaa	gag	gca	ctg	gca	gaa	aac	aac	ctg	aac	ctt	cca	aag	1254
107	Glu	Ser	Ser	Lys	Glu	Ala	Leu	Ala	Glu	Asn	Asn	Leu	Asn	Leu	Pro	Lys	
108			375				380					385					
109	atg	gct	gaa	aaa	gat	gga	tgc	ttc	caa	tct	gga	ttc	aat	gag	gag	act	1302
110	Met	Ala	Glu	Lys	Asp	Gly	Cys	Phe	Gln	Ser	Gly	Phe	Asn	Glu	Glu	Thr	
111		390				395					400						
112	tgc	ctg	gtg	aaa	atc	atc	act	ggg	ctt	ttg	gag	ttt	gag	gta	tac	cta	1350
113	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	Glu	Phe	Glu	Val	Tyr	Leu	
114	405				410				415						420		
115	gag	tac	ctc	cag	aac	aga	ttt	gag	agt	agt	gag	gaa	caa	gcc	aga	gct	1398
116	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln	Ala	Arg	Ala	
117				425				430				435					
118	gtg	cag	atg	agt	aca	aaa	gtc	ctg	atc	cag	ttc	ctg	cag	aaa	aag	gca	1446
119	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln	Lys	Lys	Ala	
120			440				445					450					
121	aag	aat	cta	gat	gca	ata	acc	acc	cct	gac	cca	acc	aca	aat	gcc	agc	1494
122	Lys	Asn	Leu	Asp	Ala	Ile	Thr	Thr	Pro	Asp	Pro	Thr	Thr	Asn	Ala	Ser	
123		455					460					465					
124	ctg	ctg	acg	aag	ctg	cag	gca	cag	aac	cag	tgg	ctg	cag	gac	atg	aca	1542
125	Leu	Leu	Thr	Lys	Leu	Gln	Ala	Gln	Asn	Gln	Trp	Leu	Gln	Asp	Met	Thr	
126	470				475				480								
127	act	cat	ctc	att	ctg	cgc	agc	ttt	aag	gag	ttc	ctg	cag	tcc	agc	ctg	1590
128	Thr	His	Leu	Ile	Leu	Arg	Ser	Phe	Lys	Glu	Phe	Leu	Gln	Ser	Ser	Leu	
129	485				490				495						500		
130	agg	gct	ctt	cgg	caa	atg	tagcatgggc	accgtcgac									1627
131	Arg	Ala	Leu	Arg	Gln	Met											
132				505													

<210> SEQ ID NO 2

<211> LENGTH: 525

<212> TYPE: PRT

<213> ORGANISM: Unknown

<400> SEQUENCE: 2

138	Met	Leu	Ala	Val	Gly	Cys	Ala	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Ala	Pro
139					-15					-10					-5	
140	Gly	Ala	Ala	Leu	Ala	Pro	Arg	Arg	Cys	Pro	Ala	Gln	Glu	Val	Ala	Arg
141		-1	1				5					10				
142	Gly	Val	Leu	Thr	Ser	Leu	Pro	Gly	Asp	Ser	Val	Thr	Leu	Thr	Cys	Pro
143		15				20					25					
144	Gly	Val	Glu	Pro	Glu	Asp	Asn	Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys

see item 7 on Erra Summary sheet

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000

TIME: 11:45:43

Input Set: I142471.RAW

145	30	35	40	45
146	Pro	Ala	Ala	Gly
147		Ser	His	Pro
148	Leu	Leu	Leu	Arg
149		Ser	Val	Gln
150	Tyr	Arg	Ala	Gly
151		Arg	Pro	Ala
152	Pro	Pro	Glu	Glu
153		Glu	Pro	Gln
154	Asn	Val	Val	Cys
155		Glu	Trp	Gly
156	Lys	Ala	Val	Leu
157		Leu	Val	Arg
158	Phe	Gln	Glu	Pro
159		Cys	Gln	Tyr
160	Gln	Leu	Ala	Val
161		Pro	Glu	Gly
162	Cys	Val	Ala	Ser
163		Ser	Ser	Val
164	Gln	Gly	Cys	Gly
165		Ile	Leu	Gln
166	Thr	Ala	Val	Ala
167		Arg	Asn	Pro
168	Pro	His	Ser	Trp
169		Asn	Ser	Ser
170	Tyr	Arg	Ala	Glu
171		Arg	Ser	Lys
172	Leu	Gln	His	His
173		Cys	Val	Ile
174	Val	Val	Gln	Leu
175		Arg	Ala	Gln
176	Glu	Trp	Ser	Pro
177		Glu	Ala	Met
178	Pro	Pro	Ala	Arg
179		Gly	Gly	Gly
180	Gly	Gly	Ser	Val
181		Glu	Pro	Val
182	Ala	Ala	Pro	His
183		Arg	Gln	Pro
184	Gln	Ile	Arg	Tyr
185		Ile	Leu	Asp
186	Cys	Asn	Lys	Ser
187		Asn	Met	Cys
188	Asn	Asn	Leu	Asn
189		Leu	Pro	Lys
190	Ser	Gly	Phe	Asn
191		Glu	Glu	Thr
192	Leu	Glu	Phe	Glu
193		Val	Tyr	Leu
194	Ser	Glu	Glu	Gln

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/142,471

 DATE: 01/28/2000
 TIME: 11:45:43

Input Set: I142471.RAW

```

195      430      435      440      445
196      Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
197      450      455      460
198      Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
199      465      470      475
200      Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
201      480      485      490
202      Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
203      495      500      505
204 <210> SEQ ID NO 3
205 <211> LENGTH: 1612
206 <212> TYPE: DNA
207 <213> ORGANISM: Unknown
208 <220> FEATURE:
209 <221> NAME/KEY: sig_peptide
210 <222> LOCATION: (34)..(90)
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (34)..(1593)
214 <220> FEATURE:
215 <221> NAME/KEY: mat_peptide
216 <222> LOCATION: (91)..(1593)
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
219      comprising two polypeptides with a mutual
220      affinity.
221 <400> SEQUENCE: 3
222      gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
223      Met Leu Ala Val Gly Cys Ala
224      -15
225      ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
226      Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
227      -10      -5      -1      1
228      cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
229      Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
230      5      10      15      20
231      gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
232      Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
233      25      30      35
234      gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
235      Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
236      40      45      50
237      agc aga tgg gct ggc atg gga agg agg ctg ctg ctg agg tgc gtg cag 294
238      Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu Arg Ser Val Gln
239      55      60      65
240      ctc cac gac tct gga aac tat tca tgc tac cgg gcc ggc cgc cca gct 342
241      Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala
242      70      75      80
243      ggg act gtg cac ttg ctg gtg gat gtt ccc ccc gag gag ccc cag ctc 390
244      Gly Thr Val His Leu Leu Val Asp Val Pro Pro Glu Glu Pro Gln Leu

```

PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/142,471

DATE: 01/28/2000
TIME: 11:45:43

Input Set: I142471.RAW

Line ? Error/Warning

Original Text
